



UNITED STATES PATENT AND TRADEMARK OFFICE

SF

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/574,333	07/21/2008	Michael Karin	UCSD-10835	5879
7590 Meden & Carroll 101 Howard Street Suite 350 San Francisco, CA 94105	09/20/2010	RECEIVED SEP 23 2010 MEDLEN & CARROLL	EXAMINER QIAN, CELINE X	ART UNIT 1636
		MAIL DATE 09/20/2010	DELIVERY MODE PAPER	

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

*Sig. Listing due 10/20/10
cc:*



UNITED STATES PATENT AND TRADEMARK OFFICE

COMMISSIONER FOR PATENTS
UNITED STATES PATENT AND TRADEMARK OFFICE
WASHINGTON, DC 20231
www.uspto.gov

APPLICATION NO. /CONTROL NO. 10574333	FILING DATE 7/21/2008	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION KARIN ET AL.	ATTORNEY DOCKET NO. UCSD-10835
--	--------------------------	--	-----------------------------------

EXAMINER
CELINE X. QIAN

ART UNIT 1636	PAPER 20100916
------------------	-------------------

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 C.F.R. § 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 C.F.R. §§ 1.821-1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

APPLICANT IS GIVEN ONE MONTH FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 C.F.R., §§ 1.821-1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 C.F.R. § 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 C.F.R. § 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

The addresses below are effective 5 June 2004. Please direct all replies to the United States Patent and Trademark Office via one (1) of the following:

1. Electronically submitted through EFS-Web (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>>, EFS Submission User Manual - ePAVE)
2. Mailed to:

Mail Stop Sequence
Commissioner for Patents
P.O. Box 22313 1450
Alexandria, VA 22313 1450
3. Hand Carry, Federal Express, United Parcel Service or other delivery service to:

U.S. Patent and Trademark Office
Mail Stop Sequence
Customer Window
Randolph Building
401 Dulany Street
Alexandria, VA 22314

Any inquiry concerning this communication should be directed to Celine Qian at telephone number (571)272-0777. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Christopher Low, can be reached on 571-272-0951

Celine X Qian
Primary Examiner
Art Unit: 1636

DETAILED ACTION

The communication filed on 7/27/2010 is not fully responsive to the Office communication mailed on 4/27/2010 for the reason(s) set forth on the attached Notice To Comply With The Sequence Rules. The computer readable version of the sequence listing has not been accepted because the description of "n" being amino acid is not acceptable. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Since the reply appears to be bona fide attempt to comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825), applicant is given a TIME PERIOD of **ONE (1) MONTH** from the mailing date of this communication within which to correct the deficiency so as to comply with the sequence rules (37 CFR 1.821 - 1.825) in order to avoid abandonment of the application under 37 CFR 1.821(g). EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

Any inquiry concerning this communication or earlier communications from the examiner should be directed to CELINE X. QIAN whose telephone number is (571)272-0777. The examiner can normally be reached on 10-6:30 M-F.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Christopher Low can be reached on 571-272-0951. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

/Celine X Qian /
Primary Examiner, Art Unit 1636

Notice to Comply	Application No. 10574333	Applicant(s) KARIN ET AL.
	Examiner CELINE X. QIAN	Art Unit 1636

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- 7. Other:

Applicant Must Provide:

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment specifically directing its entry into the application.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (571) 272-0731 or (571) 272-0951

For CRF Submission Help, call (571) 272-2510

PatentIn Software Program Support

Technical Assistance, 1-866-217-9197 or 703-305-3028 or 571-272-6845

PatentIn Software is Available At www.USPTO.gov

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

Celine X Qian Primary Examiner Art Unit: 1636	
---	--

=====

Sequence Listing could not be accepted.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan
Timestamp: [year=2010; month=7; day=27; hr=9; min=43; sec=57; ms=320;]

=====

Reviewer Comments:

<210> 57
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<222> (1)..(1)
<223> n is glycine or alanine.

<220>
<221> misc_feature
<222> (7)..(7)
<223> n is threonine or cysteine.

<220>
<221> misc_feature
<222> (8)..(8)
<223> n is threonine or cysteine.

<400> 57
nggaganntg
10

The above <220>-<223> sections describing the "n's" are errored: "n"
can only represent a single nucleotide; it cannot represent an amino

acid.

<210> 130
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> X can be a or g.

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> X can be t or c.

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> X can be a or g.

<400> 130

Xaa Gly Gly Ala Gly Ala Xaa Thr Thr Xaa
1 5 10

If the above <220>-<223> sections regarding the "Xaa's" are defining them as nucleotides, they are erroneous. If they are denoting amino acids, please spell them out in the <223> responses.

Application No: 10574333

Version No: 1.0

Input Set:

Output Set:

Started: 2010-07-21 14:54:12.726
Finished: 2010-07-21 14:54:16.948
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 222 ms
Total Warnings: 100
Total Errors: 0
No. of SeqIDs Defined: 134
Actual SeqID Count: 134

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)
W 213	Artificial or Unknown found in <213> in SEQ ID (35)
W 213	Artificial or Unknown found in <213> in SEQ ID (36)
W 213	Artificial or Unknown found in <213> in SEQ ID (37)
W 213	Artificial or Unknown found in <213> in SEQ ID (38)
W 213	Artificial or Unknown found in <213> in SEQ ID (39)
W 213	Artificial or Unknown found in <213> in SEQ ID (40)

Input Set:

Output Set:

Started: 2010-07-21 14:54:12.726
Finished: 2010-07-21 14:54:16.948
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 222 ms
Total Warnings: 100
Total Errors: 0
No. of SeqIDs Defined: 134
Actual SeqID Count: 134

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> The Regents of the University of California
Karin, Michael
Bonizzi, Giussepina
Bebien, Mahali

<120> Compositions and Methods for Gene Expression

<130> UCSD-10835

<140> 10574333

<141> 2010-07-21

<150> US 60/508349

<151> 2003-10-01

<150> PCT/US2004/032246

<151> 2004-09-29

<160> 134

<170> PatentIn version 3.5

<210> 1

<211> 700

<212> DNA

<213> Mus musculus

<400> 1	
ttcggtaccat ccacccaccc ccagtcgaga gaataggggt acagagggga ggtggcaaag	60
aaaatttacgt atactgatca tctctgggg acctgtttgg tctctttgtc cggtagcgcga	120
gcccacgtt agaatgcate ttccccggaa tgactgttagt gagactttgg ctggaaatcc	180
agtttattctt aactgttagat tggtccacgt tgccctaamc ctagcagtcc actgcggcac	240
agacacccctg gacatgaggt gggtcacgtt aagttcttg cacaagaa agggtactct	300
ggcaactttt ggatggggcg aaacacactg ttctgtctt cagtttctta ttcaacggct	360
tgtgccttgc acagcccccgtt agtttcttca tctgcaggat gggagcatta agctctacga	420
ccccacccctt ttacaattca ggtccaaaga gcccccccaa gtttggggact gggaaatca	480
aaggctctcg caccctcgccg agcccgccgcg actggggcg ccaaaaggd ggtgggttagg	540
tagggactcg gaaaggccgcg tgctccgcag gggatgcgcq tcagagaccc cagccacact	600
ccaggccccccgc cccttgcgtca gcccccccccc gccccgcctg gttttcgcct ctaaaagcgcc	660
cagcgctcgcg cttcccgctgc cgacttca ctctgggtcc	700

<210> 2

<211> 10
<212> DNA
<213> Mus musculus

<400> 2
gggagacctg 10

<210> 3
<211> 933
<212> PRT
<213> Homo sapiens

<400> 3

Met Glu Ser Cys Tyr Asn Pro Gly Leu Asp Gly Ile Ile Glu Tyr Asp
1 5 10 15

Asp Phe Lys Leu Asn Ser Ser Ile Val Glu Pro Lys Glu Pro Ala Pro
20 25 30

Glu Thr Ala Asp Gly Pro Tyr Leu Val Ile Val Glu Gln Pro Lys Gln
35 40 45

Arg Gly Phe Arg Phe Arg Tyr Gly Cys Glu Gly Pro Ser His Gly Gly
50 55 60

Leu Pro Gly Ala Ser Ser Glu Lys Gly Arg Lys Thr Tyr Pro Thr Val
65 70 75 80

Lys Ile Cys Asn Tyr Glu Gly Pro Ala Lys Ile Glu Val Asp Leu Val
85 90 95

Thr His Ser Asp Pro Pro Arg Ala His Ala His Ser Leu Val Gly Lys
100 105 110

Gln Cys Ser Glu Leu Gly Ile Cys Ala Val Ser Val Gly Pro Lys Asp
115 120 125

Met Thr Ala Gln Phe Asn Asn Leu Gly Val Leu His Val Thr Lys Lys
130 135 140

Asn Met Met Gly Thr Met Ile Gln Lys Leu Gln Arg Gln Arg Leu Arg
145 150 155 160

Ser Arg Pro Gln Gly Leu Thr Glu Ala Glu Gln Arg Glu Leu Glu Gln
165 170 175

Glu Ala Lys Glu Leu Lys Val Met Asp Leu Ser Ile Val Arg Leu
180 185 190

Arg Phe Ser Ala Phe Leu Arg Ala Ser Asp Gly Ser Phe Ser Leu Pro
195 200 205

Leu Lys Pro Val Thr Ser Gln Pro Ile His Asp Ser Lys Ser Pro Gly
210 215 220

Ala Ser Asn Leu Lys Ile Ser Arg Met Asp Lys Thr Ala Gly Ser Val
225 230 235 240

Arg Gly Gly Asp Glu Val Tyr Leu Leu Cys Asp Lys Val Gln Lys Asp
245 250 255

Asp Ile Glu Val Arg Phe Tyr Glu Asp Asp Glu Asn Gly Trp Gln Ala
260 265 270

Phe Gly Asp Phe Ser Pro Thr Asp Val His Lys Gln Tyr Ala Ile Val
275 280 285

Phe Arg Thr Pro Pro Tyr His Lys Met Lys Ile Glu Arg Pro Val Thr
290 295 300

Val Phe Leu Gln Leu Lys Arg Lys Arg Gly Asp Val Ser Asp Ser
305 310 315 320

Lys Gln Phe Thr Tyr Tyr Pro Leu Val Glu Asp Lys Glu Glu Val Gln
325 330 335

Arg Lys Arg Arg Lys Ala Leu Pro Thr Phe Ser Gln Pro Phe Gly Gly
340 345 350

Gly Ser His Met Gly Gly Ser Gly Gly Ala Ala Gly Gly Tyr Gly
355 360 365

Gly Ala Gly Gly Ser Leu Gly Phe Phe Pro Ser Ser Leu Ala
370 375 380

Tyr Ser Pro Tyr Gln Ser Gly Ala Gly Pro Met Arg Cys Tyr Pro Gly
385 390 395 400

Gly Gly Gly Ala Gln Met Ala Ala Thr Val Pro Ser Arg Asp Ser
405 410 415

Gly Glu Glu Ala Ala Glu Pro Ser Ala Pro Ser Arg Thr Pro Gln Cys
420 425 430

Glu Pro Gln Ala Pro Glu Met Leu Gln Arg Ala Arg Glu Tyr Asn Ala
435 440 445

Arg Leu Phe Gly Leu Ala His Ala Ala Pro Ser Pro Thr Arg Leu Leu
450 455 460

Arg His Arg Gly Arg Arg Ala Leu Leu Ala Gly Gln Arg His Leu Leu
465 470 475 480

Thr Ala Gln Asp Glu Asn Gly Asp Thr Pro Leu His Leu Ala Ile Ile
485 490 495

His Gly Gln Thr Ser Val Ile Glu Gln Ile Val Tyr Val Ile His His
500 505 510

Ala Gln Asp Leu Gly Val Val Asn Leu Thr Asn His Leu His Gln Thr
515 520 525

Pro Leu His Leu Ala Val Ile Thr Gly Gln Thr Ser Val Val Ser Phe
530 535 540

Leu Leu Arg Val Gly Ala Asp Pro Ala Leu Leu Asp Arg His Gly Asp
545 550 555 560

Ser Ala Met His Leu Ala Leu Arg Ala Gly Ala Gly Ala Pro Glu Leu
565 570 575

Leu Arg Ala Leu Leu Gln Ser Gly Ala Pro Ala Val Pro Gln Leu Leu
580 585 590

His Met Pro Asp Phe Glu Gly Leu Tyr Pro Val His Leu Ala Val Arg
595 600 605

Ala Arg Ser Pro Glu Cys Leu Asp Leu Leu Val Asp Ser Gly Ala Glu
610 615 620

Val Glu Ala Thr Glu Arg Gln Gly Gly Arg Thr Ala Leu His Leu Ala
625 630 635 640

Thr Glu Met Glu Glu Leu Gly Leu Val Thr His Leu Val Thr Lys Leu
645 650 655

Arg Ala Asn Val Asn Ala Arg Thr Phe Ala Gly Asn Thr Pro Leu His
660 665 670

Leu Ala Ala Gly Leu Gly Tyr Pro Thr Leu Thr Arg Leu Leu Leu Lys
675 680 685

Ala Gly Ala Asp Ile His Ala Glu Asn Glu Glu Pro Leu Cys Pro Leu
690 695 700

Pro Ser Pro Pro Thr Ser Asp Ser Asp Ser Glu Gly Pro Glu
705 710 715 720

Lys Asp Thr Arg Ser Ser Phe Arg Gly His Thr Pro Leu Asp Leu Thr
725 730 735

Cys Ser Thr Leu Val Lys Thr Leu Leu Leu Asn Ala Ala Gln Asn Thr
740 745 750

Met Glu Pro Pro Leu Thr Pro Pro Ser Pro Ala Gly Pro Gly Leu Ser
755 760 765

Leu Gly Asp Thr Ala Leu Gln Asn Leu Glu Gln Leu Leu Asp Gly Pro
770 775 780

Glu Ala Gln Gly Ser Trp Ala Glu Leu Ala Glu Arg Leu Gly Leu Arg
785 790 795 800

Ser Leu Val Asp Thr Tyr Arg Gln Thr Thr Ser Pro Ser Gly Ser Leu
805 810 815

Leu Arg Ser Tyr Glu Leu Ala Gly Gly Asp Leu Ala Gly Leu Leu Glu
820 825 830

Ala Leu Ser Asp Met Gly Leu Glu Glu Gly Val Arg Leu Leu Arg Gly
835 840 845

Pro Glu Thr Arg Asp Lys Leu Pro Ser Thr Glu Val Lys Glu Asp Ser

850

855

860

Ala Tyr Gly Ser Gln Ser Val Glu Gln Glu Ala Glu Lys Leu Gly Pro
865 870 875 880

Pro Pro Glu Pro Pro Gly Gly Leu Ser His Gly His Pro Gln Pro Gln
885 890 895

Val Thr Asp Leu Leu Pro Ala Pro Ser Pro Leu Pro Gly Pro Pro Val
900 905 910

Gln Arg Pro His Leu Phe Gln Ile Leu Phe Asn Thr Pro His Pro Pro
915 920 925

Leu Ser Trp Asp Lys
930

<210> 4
<211> 3001
<212> DNA
<213> Homo sapiens

<400> 4
actttctgc ccccccggc gccaagccca actccggatc tcgtcttcca ccggatctca 60

cccgccacac ccggacaggc ggctggagga ggcggggcgtc taaaattctg ggaagcagaa 120

ctggccggaa gccactagac agagccgggc ctggccca gacatggaga gttgtacaa 180

cccaggctcg gatggatata ttgaaatatcg tgatttcataa ttgaactct ccattgtgga 240

accmaaggag ccagccccag aaacagctqa tggccctac ctggtgatcg tggAACAGCC 300

taaggcaga ggttcccgat ttcgatatgg ctgtggaa ggcctccatg gaggactgcc 360

cggtgcctcc agtgagaagg gccgaaagac ctatccact gtcaagatct gtaactacga 420

gggaccggc aagatcgagg tggacctgtt aaacacacgt gacccaccc tcgtcatgc 480

ccacagtctg tggggcaagg aatgtcgaa gctggggatc tgccgcgttt ctgtggggcc 540

caaggacatg actgccccat ttaacaacct gggtgtccctg catgtgacta agaagaacat 600

gtatgggact atgataaaaa aacttcagag gcagccggc tcgtcttagc cccaggccct 660

taatggggcc gacccgggg agctggggca agggccaaa gaactgaaga aggtgtatgg 720

tctgtgtata gtggggctgc gcttctgc ctggccatgg gccaggatgc gtcgttctc 780

cctggccctgc aagccaggatca ccccccggcc catccatgtat agcaaatctc cggggggatc 840

ccgacagaca	acctcaccca	gtggcagect	cctgcgeagc	tacgagctgg	ctggcgaaaa	2640
cctggcagg	tactggagg	ccctgtctga	catggcccta	gaggaggagg	tgaggtgtct	2700
gagggttcca	gaaaaccggag	acaagctgcc	cagcacagag	gtgaaggaaag	acagtgcgta	2760
cgggagccag	tcaagtggagc	aggaggccaga	gaagctgggc	ccacccccctg	agccaccagg	2820
agggtctcg	cacggggcacc	cccaagctca	ggtgactgac	ctgctgcctg	cccccaagccc	2880
cetttccgga	ccccctgtac	agcggtccca	cctatttca	atcttattta	acacccwaca	2940
cccacccctc	agtgggaca	aataaaggat	tctcatggga	agggaggac	cccgaaatcc	3000
t						3001

<210> 5
<211> 899
<212> PRT
<213> Mus musculus

<400> 5

Met	Asp	Asn	Cys	Tyr	Asp	Pro	Gly	Leu	Asp	Gly	Ile	Pro	Glu	Tyr	Asp
1					5			10				15			

Asp	Phe	Glu	Phe	Ser	Pro	Ser	Ile	Val	Glu	Pro	Lys	Asp	Pro	Ala	Pro
					20			25			30				

Glu	Thr	Ala	Asp	Gly	Pro	Tyr	Leu	Val	Ile	Val	Glu	Gln	Pro	Lys	Gln
								35			40			45	

Arg	Gly	Phe	Arg	Phe	Arg	Tyr	Gly	Cys	Glu	Gly	Pro	Ser	His	Gly	Gly
					50			55			60				

Leu	Pro	Gly	Ala	Ser	Ser	Glu	Lys	Gly	Arg	Lys	Thr	Tyr	Pro	Thr	Val
65					70				75			80			

Lys	Ile	Cys	Asn	Tyr	Glu	Gly	Pro	Ala	Lys	Ile	Glu	Val	Asp	Leu	Val
					85				90			95			

Thr	His	Ser	Asp	Pro	Pro	Arg	Ala	His	Ala	His	Ser	Leu	Val	Gly	Lys
					100			105			110				

Gln	Cys	Ser	Glu	Leu	Gly	Val	Cys	Ala	Val	Ser	Val	Gly	Pro	Lys	Asp
					115			120			125				

Met Thr Ala Gln Phe Asn Asn Leu Gly Val Leu His Val Thr Lys Lys

130 135 140

Asn Met Met Glu Ile Met Ile Gln Lys Leu Gln Arg Gln Arg Leu Arg

145 150 155 160

Ser Lys Pro Gln Gly Leu Thr Glu Ala Glu Arg Arg Glu Leu Glu Gln

165 170 175

Glu Ala Lys Glu Leu Lys Lys Val Met Asp Leu Ser Ile Val Arg Leu

180 185 190

Arg Phe Ser Ala Phe Leu Arg Ala Ser Asp Gly Ser Phe Ser Leu Pro

195 200 205

Leu Lys Pro Val Ile Ser Gln Pro Ile His Asp Ser Lys Ser Pro Gly

210 215 220

Ala Ser Asn Leu Lys Ile Ser Arg Met Asp Lys Thr Ala Gly Ser Val

225 230 235 240

Arg Gly Gly Asp Glu Val Tyr Leu Leu Cys Asp Lys Val Gln Lys Asp

245 250 255

Asp Ile Glu Val Arg Phe Tyr Glu Asp Asp Glu Asn Gly Trp Gln Ala

260 265 270

Phe Gly Asp Phe Ser Pro Thr Asp Val His Lys Gln Tyr Ala Ile Val

275 280 285

Phe Arg Thr Pro Pro Tyr His Lys Met Lys Ile Glu Arg Pro Val Thr

290 295 300

Val Phe Leu Gln Leu Lys Arg Lys Arg Gly Asp Val Ser Asp Ser

305 310 315 320

Lys Gln Phe Thr Tyr Tyr Pro Leu Val Glu Asp Lys Glu Glu Val Gln

325 330 335

Arg Lys Arg Arg Lys Ala Leu Pro Thr Phe Ser Gln Pro Phe Gly Gly

340 345 350

Gly Ser His Met Gly Gly Ser Gly Gly Ser Ala Gly Gly Tyr Gly

355

360

365

Gly Ala Gly Gly Gly Ser Leu Gly Phe Phe Ser Ser Ser Leu Ala
370 375 380

Tyr Asn Pro Tyr Gln Ser Gly Ala Ala Pro Met Gly Cys Tyr Pro Gly
385 390 395 400

Gly Gly Gly Ala Gln Met Ala Gly Ser Arg Arg Asp Thr Asp Ala
405 410 415

Gly Glu Gly Ala Glu Glu Pro Arg Thr Pro Pro Glu Ala Pro Gln Gly
420 425 430

Glu Pro Gln Ala Leu Asp Thr Leu Gln Arg Ala Arg Glu Tyr Asn Ala
435 440 445

Arg Leu Phe Gly Leu Ala Gln Arg Ser Ala Arg Ala Leu Leu Asp Tyr
450 455 460

Gly Val Thr Ala Asp Ala Arg Ala Leu Leu Ala Gly Gln Arg His Leu
465 470 475 480

Leu Met Ala Gln Asp Glu Asn Gly Asp Thr Pro Leu His Leu